Amendments to the Claims:

This listing of claims will replace all prior versions and listings of claims in the application.

Please amend claims 1-14, 16, 24-25, 36, and 38.

Claims 17-21 are cancelled without prejudice.

Claims 39-56 are newly presented herein.

Claim 1. (Currently Amended) An isolated nucleic acid comprising nucleic acids selected from the group consisting of:

an isolated polynucleotide comprising the sequence of SEQ ID NO:1,

an isolated erythrovirus V9 variant genome, wherein said variant displays less than or equal to 6% genetic relatedness as compared to the prototypical isolate of SEQ ID NO:1 and greater than or equal to 10% genetic relatedness as compared to the prototypical B19 isolate; and ~~the genomic sequences of variant erythroviruses, called erythrovirus type V9, which, molecularly, cannot be recognized as an erythrovirus B19 because it exhibits a genetic divergence ≥10% over the whole genome with respect to the erythrovirus B19 sequences and which exhibit a genetic divergence of less than or equal to 6% with respect to the sequence SEQ ID NO:1; and~~

an isolated full-length erythroviral genomic nucleic acid comprising a nucleotide sequence which hybridizes under stringent conditions of hybridization for 3 to 24 hours in a 1XSSC buffer containing 50% formamide at 42°C and three washes of 15 minutes in a 2XSSC buffer at 60°C with SEQ ID NO:1; and

an isolated full-length erythroviral ~~the erythrovirus~~ genomic nucleic acid comprising a nucleotide sequence ~~sequences~~ which ~~hybridize~~ hybridizes under stringent conditions of~~,~~ hybridization for 3 to 24 hours in a 1XSSC buffer containing 50% formamide at 42°C and three washes of 15 minutes in a 2XSSC buffer at 60°C with ~~one of the following sequences~~ a polynucleotide sequence consisting of~~:~~ SEQ ID NO:45-80, SEQ ID NO:81, SEQ ID NO:83, SEQ ID NO:85, SEQ ID NO:87, SEQ ID NO:89, SEQ ID NO:91, SEQ ID NO:93, SEQ ID NO:108, SEQ ID NO:110, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119 or ~~and~~ SEQ ID NO:120.

Claim 2. (Currently Amended) The isolated nucleic acid of Claim 1 wherein the nucleic acid exhibits a restriction profile according to Figures 7.1 to 7.3.

Claim 3. (Currently Amended) An isolated nucleic acid fragment comprising ~~Fragments of the nucleic acids according to Claim 1 selected from the group consisting of~~:

a) a sequence comprising at least 17 nucleotides of ~~the sequences~~ SEQ ID NO:81, SEQ ID NO:83, SEQ ID NO:85, SEQ ID NO:87, SEQ ID NO:89, SEQ ID NO:91 or SEQ ID NO:93,

b) a sequence comprising at least 17 nucleotides of ~~the sequences~~ SEQ ID NO:2-80,

c) a sequence comprising at least 17 nucleotides of ~~the sequences~~ SEQ ID NO: 105-121, and

d) a sequence comprising at least 17 nucleotides of a sequence ~~the sequences~~ complementary to any of a), b), or c) ~~the preceding sequences of parts 3a) 3c), wherein the fragments comprise at least 17 nucleotides derived from the preceding sequences or their complementary sequences~~.

Claim 4. (Currently Amended) The fragment according to Claim 3, wherein the fragment comprises at least 17 nucleotides of ~~selected from the group consisting of the sequences~~ SEQ ID NO:45-80, 108 AND NO:110 or a complement thereof ~~their complementary sequences, the sequences of at least 17 nucleotides derived from these sequences and the sequences comprising the said sequences and wherein the selected sequence serves as a probe in the specific identification of an erythrovirus V9 or of a related erythrovirus~~.

Claim 5. (Currently Amended) The fragment according to Claim 3, wherein the fragment comprises at least 17 nucleotides of ~~selected form the group consisting of the sequences~~ SEQ ID NO:2-80, ~~and the sequences~~ SEQ ID NO: 105-121, or a complement thereof ~~their complementary sequences, the sequences of at least 17 nucleotides derived from these sequences and the sequences comprising the said sequences and wherein the selected sequence serves as a~~

~~primer for the amplification of sequences derived from an erythrovirus~~.

Claim 6. (Currently Amended): A pair of primers selected from the group consisting of:

pair A: primers comprising SEQ ID NO:111 and SEQ ID NO:112;

pair B: primers comprising SEQ ID NO:105 and SEQ ID NO:106;

pair C: a first primer comprising one of the sequences SEQ ID NO:2-44, 105, 106, 107, 109, 111 or 112 and a second primer comprising one of the sequences SEQ ID NO:45-80, 108 or 110;

pair D: primers comprising SEQ ID NO:107 and SEQ ID NO:109;

pair E: two primers comprising a sequence of ~~selected from the sequences~~ SEQ ID NO:2-44, 105, 106, 107, 109, 111 or 112; and

pair F: two primers comprising a sequence of ~~selected from the sequences~~ SEQ ID NO:45-80, 108 or 110.

Claim 7. (Currently Amended): ~~A~~ An isolated variant erythrovirus, wherein said variant displays less than or equal to 6% genetic relatedness as compared to the prototypical V9 isolated consisting of SEQ ID NO:1 and wherein ~~which cannot be recognized molecularly as an erythrovirus B19 genome in that it exhibits a genetic divergence of less than or equal to 6% with the sequence SEQ ID:1 and in that~~ the genome of the variant erythrovirus ~~its genome~~ hybridizes specifically, under stringent conditions of hybridization for 3 to 24 hours in a 1XSSC buffer containing 50% formamide at 42°C and three washes of 15 minutes in a 2XSSC buffer at 60°C with a polynucleotide comprising a sequence of ~~one of the sequences~~ SEQ ID NO:45 to 80, 108 ~~and~~ or 110, or a complement thereof.

Claim 8. (Currently Amended): A plasmid comprising ~~the~~ a viral genome of a variant erythrovirus strain V9~~, called erythrovirus V9~~, wherein said variant displays less than or equal to 6% genetic relatedness as compared to a prototypical V9 having a genomic sequence of SEQ ID NO:1 and greater than or equal to 10% genetic relatedness as compared to the prototypical B19

isolate ~~which cannot be recognized moleculary as an erythrovirus B19 and which exhibits with the latter a genetic divergence of ≥10% over the whole genome with respect to the erythrovirus B19 sequences and a genetic divergence of less than or equal to 6% with respect to the sequence SEQ ID NO:1 or a fragment thereof, according to Claim 3~~.

Claim 9. (Currently Amended) The ~~A~~ plasmid, according to Claim 8, comprising a sequence SEQ ID NO:1.

Claim 10. (Currently Amended): A diagnostic reagent for the specific ~~differential~~ detection of type V9 erythroviruses selected from ~~the~~ fragments of nucleic acids comprising a sequence of at least 17 nucleotides of ~~sequences~~ SEQ ID NO:45-80, 108 or ~~and~~ 110, or a complement thereof ~~their complementary sequences, and the sequences of at least 17 nucleotides, derived from these sequences~~.

Claim 11. (Currently Amended): A method for ~~the rapid and~~ differential diagnosis of ~~erythroviruses,~~ erythroviral infection in a subject ~~by hybridization and/or gene amplification, using a biological sample as starting material~~, comprising:

(1) contacting a biological sample from a subject ~~to be analyzed~~ with

(a) at least one primer or probe comprising a sequence of ~~of sequence~~ SEQ ID NO:45-80, 108 or 110, and

(b) at least one primer or probe comprising a sequence of SEQ ID NO:2-44, 105, 106, 107, 109, 111 or 112; and

(2) detecting the presence or absence of product (s) resulting from

(a) specific hybridization of a V9 nucleic acid with a primer or probe of (1)(a) ~~the erythrovirus nucleotide sequence probe interaction by any appropriate means;~~

(b) specific hybridization of an erythrovirus nucleic acid with a primer or probe of (1)(b)

wherein detection of product(s) of (2)(a) indicates a diagnosis of V9 erythrovirus infection and detection of product(s) of (2)(b) indicates a diagnosis of an erythrovirus infection, thereby establishing a differential diagnosis of erythrovirus infection in the subject.

Claim 12. (Currently Amended): The method according to Claim 11 comprising, prior to step (1):

extracting ~~the~~ viral nucleic acid ~~to be detected, belonging to the virus genome,~~ which may be present in the biological sample, and

performing at least one ~~gene~~ nucleic acid amplification cycle.

Claim 13. (Currently Amended): The method according to Claim 12 wherein the amplification cycles are carried out with the aid of a pair of primers selected from the group consisting of:

pair A: primers comprising SEQ ID NO:111 and SEQ ID NO:112;

pair B: primers comprising SEQ ID NO:105 and SEQ ID NO:106;

pair C: a first primer comprising one of the sequences SEQ ID NO:2-44, 105, 106, 107, 109, 111 or 112 and a second primer comprising one of the sequences SEQ ID NO:45-80, 108 or 110;

pair D: ~~primer~~ primers comprising SEQ ID NO:107 and ~~primer~~ SEQ ID NO:109;

pair E: two primers comprising a sequence of ~~selected from the sequences~~ SEQ ID NO:2-44, 105, 106, 107, 109, 111 or 112; and

pair F: two primers comprising a sequence of ~~selected from the sequences~~ SEQ ID NO:45-80, 108 or 110.

Claim 14. (Currently Amended): A method for ~~the rapid and~~ differential detection ~~diagnosis~~ of erythroviruses comprising:

extracting ~~the~~ nucleic acid ~~to be detected, belonging to the virus genome,~~ which may be present in a ~~the~~ biological sample,

performing at least one gene amplification cycle with the aid of a pair of primers according to Claim 6, and

detecting the amplified product by hybridization to a probe comprising a sequence of SEQ ID NO:121, ~~with the sequence SEQ ID NO:121~~ by cleavage by ~~the action of the~~ restriction enzyme MunI, or both; and

comparing the length of the detected amplified product with a V9 positive control and a B19 positive control.

Claim 15. (Canceled)

Claim 16. (Currently Amended): A method of screening and typing an erythrovirus ~~V9 or a related virus~~ comprising:

~~bringing~~ contacting a probe selected from the group consisting of the sequences according to Claim 4, into contact with ~~the~~ nucleic acid of the virus to be typed, under stringent conditions of hybridization for 3 to 24 hours in a 1XSSC buffer containing 50% formamide at 42°C and three washes of 15 minutes in a 2XSSC buffer at 60°C ~~and detecting the nucleic acid probe hybrid obtained~~ and

detecting the presence of absence of a nucleic acid-probe hybrid,

wherein the presence of the nucleic acid-probe hybrid indicates the virus is a V9 erythrovirus.

Claims17-23. (Cancelled)

Claim 24. (Currently Amended): A method for the detection of an erythrovirus in an individual ~~of *in vitro* screening diagnosis of infection of an individual with an erythrovirus~~

~~comprising detecting hybridization of~~ comprising:
contacting a biological sample from an individual with at least one of a nucleic acid primer or nucleic acid probe, which primer or probe specifically hybridizes ~~the individual's nucleic acid~~ with a nucleic acid according to Claim 1; and
detecting hybridization of the primer or probe to a nucleic acid in the sample.

Claim 25. (Currently Amended): The method of claim 24, wherein said detecting comprises ~~comprising gene~~ nucleic acid-based amplification of a nucleic acid in the sample.

Claim 26. (Previously presented): The method of claim 16 wherein the probe is labeled.

Claim 27. (Previously presented): The method of claim 16 wherein the nucleic acid of the virus to be typed is labeled.

Claim 28-35. (Canceled)

Claim 36. (Currently Amended): An erythrovirus diagnostic kit comprising at least one probe comprising a sequence of ~~sequence~~ SEQ ID NO: 45-80, 108 or 110, or a primer that hybridizes to a nucleic acid sequence consisting of SEQ ID NO: 1 ~~of claim 1~~ under stringent conditions of hybridization for 3 to 24 hours in a 1XSSC buffer containing 50% formamide at 42°C and three washes of 15 minutes in a 2XSSC buffer at 60°C.

Claim 37. (Previously presented): The diagnostic reagent of claim 10 wherein the reagent is labeled with an appropriate marker.

Claim 38. (Currently Amended): The isolated nucleic acid of claim 1 comprising SEQ ID NO:1.

Claim 39. (New) A method for rapid and differential diagnosis of erythrovirus by gene amplification and hybridization, using a biological sample as starting material, comprising:

contacting a biological sample with a first pair of primers which provide for specific amplification of V9 erythrovirus nucleic acid, wherein said contacting provides for production of a first amplification product if V9 erythrovirus nucleic acid is present in the sample; and

a second pair of primers which provide for amplification of erythrovirus nucleic acid in the biological sample, wherein said contacting provides for production of a second amplification product if erythrovirus nucleic acid is present in the sample

detecting the presence or absence of the first and second amplification products; wherein detection of the second amplification product indicates the presence of an erythrovirus in the sample and detection of the first amplification product indicates the presence of a V9 erythrovirus in the sample.

Claim 40. (New) The method of claim 39, wherein said detecting comprises contacting the sample with a probe that hybridizes to the first and second amplification products.

Claim 41. (New) The method of claim 38, wherein the first pair of primers comprise a nucleotide sequence of SEQ ID NOS:45-80, 208, or 110.

Claim 42. (New) The method of claim 41, wherein the second pair of primers comprise a nucleotide sequence of SEQ ID NOS: 2-44, 105-107, 109, or 111-121.

Claim 43. (New) A method for detecting a V9 erythrovirus in a sample, the method comprising:

contacting a biological sample with a nucleic acid primer or probe, which primer or probe specifically hybridizes to a nucleic acid comprising a sequence of SEQ ID NOS: 45-80,

208, or 110 or a nucleic acid encoding a polypeptide comprising an amino acid sequence of SEQ ID NO:82, SEQ ID NO:86, SEQ ID NO:88, SEQ ID NO:92, or SEQ ID NO:95-104; detecting the presence or absence of hybridization of the primer or probe.

Claim 44. (New) The method of claim 43, wherein the primer or probe specifically hybridizes to a viral nucleic acid

Claim 45. (New) The method of claim 43, wherein said detecting of hybridization of the primer is by detecting the presence or absence of an amplification product produced by extension from the primer specifically hybridized to viral nucleic acid in the sample.

Claim 46. (New) The method of claim 43, wherein the primer or probe specifically hybridizes to a nucleic acid comprising a sequence encoding a polypeptide comprising an amino acid sequence of SEQ ID NO:82, SEQ ID NO:86, SEQ ID NO:88, or SEQ ID NO:92.

Claim 47. (New) An isolated nucleic acid encoding a polypeptide comprising at least 7 contiguous amino acids of at least one of SEQ ID NO:82, SEQ ID NO:86, SEQ ID NO:88, SEQ ID NO:92, or SEQ ID NO:95-104.

Claim 48. (New) The isolated nucleic acid of claim 47, wherein the nucleic acid encodes a polypeptide of SEQ ID NO: 82.

Claim 49. (New) The isolated nucleic acid of claim 47, wherein the nucleic acid encodes a polypeptide of SEQ ID NO: 86.

Claim 50. (New) The isolated nucleic acid of claim 47, wherein the nucleic acid encodes a polypeptide of SEQ ID NO:88.

Claim 51. (New) The isolated nucleic acid of claim 47, wherein the nucleic acid encodes a polypeptide of SEQ ID NO:92.

Claim 52. (New) A method of making a polypeptide, the method comprising:
providing for expression of a polypeptide encoded by a recombinant nucleic acid comprising a nucleotide sequence of the isolated nucleic acid of claim 42 in a host cell; and
recovering the polypeptide.

Claim 53. (New) The method of claim 51, wherein the polypeptide comprises the amino acid sequence of SEQ ID NO:86, SEQ ID NO:88, SEQ ID NO:92, or SEQ ID NO:95-104.

Claim 54. (New) The method of claim 51, wherein the polypeptide comprises the amino acid sequence of SEQ ID NO:86 or SEQ ID NO:92.

Claim 55. (New) The method of claim 54, wherein the polypeptide is recovered in a viral capsid.

Claim 56. (New) The method of claim 55, wherein the polypeptide is recovered in an empty viral capsid.